

Data analysis for genome-wide CRISPR knockout screening

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 An abbreviated version of this protocol was published in eLIFE in Aug 2020

Discovery of a molecular glue promoting CDK12-DDB1 interaction to trigger cyclin K degradation

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Detailed protocol

1. Load raw Fastq files into MAGeCK (Model-based Analysis of Genome-wide CRISPR-Cas9 Knockout, v0.5.9.2) (W. Li et al., 2014).
2. Use the "count" command to collect read counts from Fastq files and to generate the sgRNA read count table.
3. Use the "test" command to perform statistical test from the count table, outputting log₂ fold change, p value, and false discovery rate (FDR).
4. Load the result table generated by MAGeCK into ggplot2 (Wickham, 2016) in R to generate a volcano plot.

How to cite: (Readers should cite both the Bio-protocol preprint and the original research article where this protocol was used)

1. Qi, X. and Han, T. (2021). Data analysis for genome-wide CRISPR knockout screening. Bio-protocol Preprint. bio-protocol.org/prep1123.
2. Lv, L., Chen, P., Cao, L., Li, Y., Zeng, Z., Cui, Y., Wu, Q., Li, J., Wang, J., Dong, M., Qi, X. and Han, T. (2020). Discovery of a molecular glue promoting CDK12-DDB1 interaction to trigger cyclin K degradation. eLIFE. DOI: [10.7554/eLife.59994](https://doi.org/10.7554/eLife.59994)

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